

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Regents of the University of Minnesota
- (ii) TITLE OF THE INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 - (B) STREET: 3100 Norwest Center, 90 South 7th Street
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US97/22228
 - (B) FILING DATE: 05-DEC-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/032,930
 - (B) FILING DATE: 06-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Skoog, Mark T
 - (B) REGISTRATION NUMBER: 40,178
 - (C) REFERENCE/DOCKET NUMBER: 600.346WOI1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612-332-5300
 - (B) TELEFAX: 612-332-9081
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCATCACGGG TGGATTCTTG AAACAGGTG

29

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATCACGCC CCCCCTCGAC GATAAAATAG TTGCTAAGCT ACAAGCT

47

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC              172

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC              172

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC              172

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA    60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA    120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC           172

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA    60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA    120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC           172

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC              172

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA      60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA      120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC              172

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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CCATCACGGG TGGATCCTTG AACAGGTGC A                                     31

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 828...1580
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATCAGCGA	TCATCATGT	TTGACAGCTT	ATCATCGATA	AGCTTACTTT	TCGAATCAGG	60
TCTATCCTTG	AAACAGGTGC	AACATAGATT	AGGGCATGGA	GATTTACCAG	ACAACTATGA	120
ACGTATATAC	TCACATCAGC	CAATCGGCAA	TTGATGACAT	TGGAACATAA	TTCAATCAAT	180
TTGTTACTAA	CAAGCAACTA	GATTGACAAC	TAATTCTCAA	CAAACGTTAA	TTTACAACA	240
TTCAAGTAAC	TCCCACCAGC	TCCATCAATG	CTTACCGTAA	GTAATCATAA	CTTACTAAAA	300
CCTTGTTACA	TCAAGGTTTT	TTCTTTTTGT	CTTGTTTCATG	AGTTACCATA	ACTTTCTATA	360
TTATTGACAA	CTAAATTGAC	AACTCTTCAA	TTATTTTTCT	GTCTACTCAA	AGTTTTCTTC	420
ATTTGATATA	GTCTAATTCC	ACCATCACTT	CTTCCACTCT	CTCTACCGTC	ACAACTTCAT	480
CATCTCTCAC	TTTTTCGTGT	GGTAACACAT	AATCAAATAT	CTTTCCGTTT	TTACGCACTA	540
TCGCTACTGT	GTCACCTAAA	ATATACCCCT	TATCAATCGC	TTCTTTAAAC	TCATCTATAT	600
ATAACATATT	TCATCCTCCT	ACCTATCTAT	TCGTAAAAAG	ATAAAAATAA	CTATTGTTTT	660
TTTTGTTATT	TTATAATAAA	ATTATTAATA	TAAGTTAATG	TTTTTTAAAA	ATATACAATT	720
TTATTCTATT	TATAGTTAGC	TATTTTTTCA	TTGTTAGTAA	TATTGGTGAA	TTGTAATAAC	780
CTTTTAAAT	CTAGAGGAGA	ACCCAGATAT	AAAATGGAGG	AATATTA ATG	GAA AAC	836
				Met Glu Asn		
				1		
AAT AAA AAA	GTA TTG AAG AAA	ATG GTA TTT TTT	GTT TTA GTG ACA	TTT		884
Asn Lys Lys	Lys Val Leu Lys	Lys Lys Met Val	Phe Phe Val	Leu Val Thr	Phe	
5		10		15		
CTT GGA CTA	ACA ATC TCG CAA	GAG GTA TTT GCT	CAA CAA GAC	CCC GAT		932
Leu Gly Leu	Thr Ile Ser Gln	Glu Val Phe Ala	Gln Gln Asp	Pro Asp		
20		25		30		
					35	

CCA AGC CAA CTT CAC AGA TCT AGT TTA GTT AAA AAC CTT CAA AAT ATA Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile 40 45 50	980
TAT TTT CTT TAT GAG GGT GAC CCT GTT ACT CAC GAG AAT GTG AAA TCT Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser 55 60 65	1028
GTT GAT CAA CTT TTA TCT CAC CAT TTA ATA TAT AAT GTT TCA GGG CCA Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro 70 75 80	1076
AAT TAT GAT AAA TTA AAA ACT GAA CTT AAG AAC CAA GAG ATG GCA ACT Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr 85 90 95	1124
TTA TTT AAG GAT AAA AAC GTT GAT ATT TAT GGT GTA GAA TAT TAC CAT Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His 100 105 110 115	1172
CTC TGT TAT TTA TGT GAA AAT GCA GAA AGG AGT GCA TGT ATC TAC GGA Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly 120 125 130	1220
GGG GTA ACA AAT CAT GAA GGG AAT CAT TTA GAA ATT CCT AAA AAG ATA Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile 135 140 145	1268
GTC GTT AAA GTA TCA ATC GAT GGT ATC CAA AGC CTA TCA TTT GAT ATT Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile 150 155 160	1316
GAA ACA AAT AAA AAA ATG GTA ACT GCT CAA GAA TTA GAC TAT AAA GTT Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val 165 170 175	1364
AGA AAA TAT CTT ACA GAT AAT AAG CAA CTA TAT ACT AAT GGA CCT TCT Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser 180 185 190 195	1412

AAA	TAT	GAA	ACT	GGA	TAT	ATA	AAG	TTC	ATA	CCT	AAG	AAT	AAA	GAA	AGT	1460
Lys	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Pro	Lys	Asn	Lys	Glu	Ser	
				200					205					210		

TTT TGG TTT GAT TTT TTC CCT GAA CCA GAA TTT ACT CAA TCT AAA TAT 1508
Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr
215 220 225

CTT ATG ATA TAT AAA GAT AAT GAA ACG CTT GAC TCA AAC ACA AGC CAA 1556
Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln
230 235 240

ATT GAA GTC TAC CTA ACA ACC AAG TAACTTTTGT CTTTGGCAA CCTTACCTAC 1610
Ile Glu Val Tyr Leu Thr Thr Lys
245 250

TGCTGGATT	AGAAATTTT	TTGCAATTCT	TTTATTAATG	TAAAAACCGC	TCATTTGATG	1670
AGCGGTTTT	TCTTATCTAA	AGGAGCTTTA	CCTCCTAATG	CTGCAAAATT	TTAAATGTTG	1730
GATTTTGTG	TTTGTCTATT	GTAATTTGATG	GGTAATCCCA	TTTTTCGACA	GACATCGTCG	1790
TGCCACCTCT	AACACCAAAA	TCATAGACAG	GAGCTTGTAG	CTTAGCAACT	ATTTTATCGT	1850
C						1851

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Met Glu Asn Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu
 1          5          10          15
Val Thr Phe Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln
 20          25          30          35
Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu
 40          45          50          55
Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn
 60          65          70          75
Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val
 80          85          90          95
Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu
100          105          110          115
Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
120          125          130          135
Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
140          145          150          155
Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
160          165          170          175
Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
180          185          190          195
Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
200          205          210          215
Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
220          225          230          235
Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
240          245          250
Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln
251
Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn
252
Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
253

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